

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 14:39:43 ; Search time 26.8 Seconds
(without alignments)
1207.091 Million cell updates/sec

Title: US-09-811-118-1
Perfect score: 187
Sequence: 1 MVAATVAAAMLILMAACAQ.....VRLQITLVKRLILKREDL 187

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp-phage:*
10: sp_plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	55.6	187	4	Q96S14
2	41	21.9	186	11	Q991J6
3	41	21.9	186	11	Q991J6
4	35	18.7	147	11	Q9CXM6
5	13	7.0	209	11	Q9D111
6	10	5.3	160	16	Q9D7B7
7	10	5.3	236	10	Q9A7J3
8	9	4.8	93	5	Q24296
9	9	4.8	98	6	Q9NM13
10	9	4.8	98	6	Q9NM13
11	9	4.8	116	10	Q9MT09
12	9	4.8	165	10	Q38703
13	9	4.8	169	10	Q9SME4
14	9	4.8	169	10	Q48646
15	9	4.8	169	10	Q9FXS3
16	9	4.8	170	10	Q24031
					Q24031 lycopersico
					Q49069 gossypium h
					Q91EFO mesembryant

17	9	4.8	170	11	Q9JHM1	Q9JHM1 cavia porce
18	9	4.8	170	11	Q9JK35	Q9JK35 mus musculu
19	9	4.8	171	10	Q23814	Q23814 spinacia ol
20	9	4.8	173	10	Q9LYB4	Q9LYB4 arabidopsis
21	9	4.8	192	10	Q9SH32	Q9SH32 arabidopsis
22	9	4.8	197	6	Q9N2J2	Q9N2J2 bos taurus
23	9	4.8	197	11	Q35560	Q35560 mus musculu
24	9	4.8	206	10	Q22850	Q22850 arabidopsis
25	9	4.8	230	10	Q9S254	Q9S254 arabidopsis
26	9	4.8	232	10	Q9ABV3	Q9ABV3 arabidopsis
27	9	4.8	236	8	Q19985	Q19985 arabidopsis
28	9	4.8	236	10	Q81717	Q81717 arabidopsis
29	9	4.8	237	10	Q9SME6	Q9SME6 hordeum vul
30	9	4.8	244	10	Q65156	Q65156 zantedesch
31	9	4.8	253	11	Q91XR9	Q91XR9 mus musculu
32	9	4.8	257	11	Q91XR8	Q91XR8 rattus norv
33	9	4.3	169	10	Q9FEV2	Q9FEV2 oryza sativ
34	8	4.3	169	10	Q04922	Q04922 arabidopsis
35	8	4.3	171	10	Q9SL86	Q9SL86 arabidopsis
36	8	4.3	171	10	Q9SME5	Q9SME5 hordeum vul
37	8	4.3	193	5	Q21666	Q21666 caenorhabdi
38	8	4.3	200	12	Q9J5E7	Q9J5E7 fowlpox vir
39	8	4.3	230	16	Q92KT2	Q92KT2 rhizodium m
40	8	4.3	348	8	Q9TD43	Q9TD43 rivulus agl
41	8	4.3	412	2	Q9AH99	Q9AH99 streptococc
42	8	4.3	412	2	Q9X9A9	Q9X9A9 streptococc
43	8	4.3	449	16	Q9PDK4	Q9PDK4 xyella fas
44	8	4.3	508	16	Q9J2W1	Q9J2W1 neisseria m
45	8	4.3	508	16	Q9JUX5	Q9JUX5 neisseria m

ALIGNMENTS

RESULT 1
ID Q96S14 PRELIMINARY: PRT: 187 AA.
AC Q96S14:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FL141477 FIS, CLONE NT2RP4000259, WEAKLY SIMILAR TO
DE GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Iisogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai Y., Saio K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuno Y., Sasaki N.,
RT "NEBO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027683; BAB5294.1; -
SQ SEQUENCE 187 AA; 20996 MW; 0ACB80AC2522EPCD CRC64;

Query Match 55.6%; Score 104; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.5e-100;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVAATVAAAMLILMAACAQEDPFDFAVNRKGLVSLKRGVSILVNVNASCGRPT 60
DB 1 MVAATVAAAMLILMAACAQEDPFDFAVNRKGLVSLKRGVSILVNVNASCGRPT 60
QY 61 DGHYRALQDLQDLPGRHFNVLAFPCNPGGOODEPDSNKETESPA 104
DB 61 DGHYRALQDLQDLPGRHFNVLAFPCNPGGOODEPDSNKETESPA 104

RESULT 2

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Q99LJ6
ID Q99LJ6 PRELIMINARY; PRT; 186 AA.
AC Q99LJ6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 3110050F08RIK.
GN SMILAR TO RIKEN CDNA 3110050F08 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANIMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;
RC Strausberg R.;
RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003228; AAH03228.1; -.
DR HSSP: P00435; 1GP1.
DR MGD: MGI:1914555; 3110050F08RIK.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PRO1011; GLUTPROXDAE.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
SQ SEQUENCE 186 AA; 21061 MW; D20211218380A1BA CRC64;

Query Match 21.9%; Score 41; DB 11; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EODFYDFKAVNIRKGLVSEKRGVSLVNVNASECGFTDQ 62
DB 21 EODFYDFKAVNIRKGLVSEKRGVSLVNVNASECGFTDQ 61

RESULT 3
Q9CXN6 PRELIMINARY; PRT; 225 AA.
AC Q9CXN6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 3110050F08RIK PROTEIN.
GN 3110050F08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
*Functional annotation of a full-length mouse cDNA collection.*;
RT
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RL Nature 409:685-690(2001).
DR EMBL: AK014199; BAB29201.1; -.
DR HSSP: P00435; 1GP1.
DR MGD: MGI:1914555; 3110050F08RIK.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam: PF00255; GSHpx; 1.
DR PRINTS: PRO1011; GLUTPROXDAE.
DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
SQ SEQUENCE 225 AA; 25606 MW; F3D7CEA1B4D22E06 CRC64;

Query Match 21.9%; Score 41; DB 11; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-34;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EODFYDFKAVNIRKGLVSEKRGVSLVNVNASECGFTDQ 62
DB 21 EODFYDFKAVNIRKGLVSEKRGVSLVNVNASECGFTDQ 61

RESULT 4
Q9D111 PRELIMINARY; PRT; 147 AA.
AC Q9D111;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 3110050F08RIK PROTEIN.
GN 3110050F08RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
*Functional annotation of a full-length mouse cDNA collection.*;
RT

QY 28 FKAVNIRKGLVSEKRGVSLVNVNASECGFTDQ 62
Query Match 18.7%; Score 35; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 27 FKAVINRGKLVSEKRYGSVLYVNVASCEGFTDQ 61

RESULT 5

ID 09D7B7 PRELIMINARY; PRT; 209 AA.

AC 09D7B7; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE 2310016C16RIK PROTEIN.

GN 2310016C16RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TONGUE;

RX MEDLINE=21085660; PubMed=11217851;

RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gliszi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL: AK009378; BAB26254.1; -

DR HSSP: P00435; 1GPI. -

DR MGD: MGI:1916840; 2310016C16RIK.

DR InterPro: IPR000889; Glut_peroxidase.

DR Pfam: PF00255; GSHpx; 1.

DR PRINTS: PR01011; GLUTPROXDAE.

DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.

SO SEQUENCE 209 AA; 24148 MW; 8DA93ED11B4ECF21 CRC64;

Query Match 7.0%; Score 13; DB 11; Length 209;

Best Local Similarity 100.0%; Pred. No. 3.2e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 HENVLAFCPCNOFG 90

DB 100 HENVLAFCPCNOFG 112

RESULT 6

ID 09A7J3 PRELIMINARY; PRT; 160 AA.

AC 09A7J3; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE GLUTATHIONE PEROXIDASE.

GN CCI730.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OX NCBI_TaxID=69394;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Pollock A., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Usterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of *Caulobacter crescentus*.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL: AE005847; AAK23706.1; -

DR HSSP: P00435; 1GPI.

DR TIGR: CCI730; -

DR InterPro: IPR000889; Glut_peroxidase.

DR Pfam: PF00255; GSHpx; 1.

DR PRINTS: PR01011; GLUTPROXDAE.

DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.

DR Peroxidase; Complete proteome.

SO SEQUENCE 160 AA; 17653 MW; 0180F8B07A06D731 CRC64;

Query Match 5.3%; Score 10; DB 16; Length 160;

Best Local Similarity 100.0%; Pred. No. 0.034;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFPCNOFG 90

DB 60 VLAFPCNOFG 69

RESULT 7

ID 024296 PRELIMINARY; PRT; 236 AA.

AC 024296; 01-JAN-1998 (TREMblrel. 05, Created)

DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI_TaxID=3888;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. BIRTE; PubMed=9680987;

RX MEDLINE=98345965; PubMed=9680987;

RA Mullineaux P.M., Karpinski S., Jimenez A., Cleary S.P., Robinson C., Creissen G.P.;

RT "Identification of cDNAs encoding plastid-targeted glutathione peroxidase.";

RL Plant J. 13:375-379(1998).

CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED GLUTATHIONE + 2 H(2)O.

CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

DR EMBL: AJ000508; CA004142.1; -

DR HSSP: P00435; 1GPI.

DR InterPro: IPR000889; Glut_peroxidase.

DR Pfam: PF00255; GSHpx; 1.

DR PRINTS: PR01011; GLUTPROXDAE.

DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.

DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.

KW Oxidoreductase; Peroxidase.

SO SEQUENCE 236 AA; 26400 MW; 85300731A34555D CRC64;

Query Match 5.3%; Score 10; DB 10; Length 236;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 VLAFPCNOFG 90
 |||||||||
 DB 135 VLAFPCNOFG 144

RESULT 8
 ID Q9NM13 PRELIMINARY; PRT; 93 AA.
 AC Q9NM13;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9) (FRAGMENT).
 GN LM26.279.
 OS Leishmania major.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajadream M., Ivens A., Barrell B.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
 GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AL160493; CAB97897.1; -.
 DR HSSP: P00435; IGPI
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPEROXDASE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KM Oxidoreductase; Peroxidase.
 FT NON_TER 93
 SQ SEQUENCE 93 AA; 10437 MW; BA59FE4D7F3910E0 CRC64;

Query Match 4.8%; Score 9; DB 5; Length 93;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 VLAFPCNOFG 89
 |||||||||
 DB 62 VLAFPCNOFG 70

RESULT 9
 ID Q9MYU9 PRELIMINARY; PRT; 98 AA.
 AC Q9MYU9;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9) (FRAGMENT).
 GN PHP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID;
 RX MEDLINE=20422104; PubMed=10964405;
 RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,

RA Christophe D.;
 RT "A method for the large-scale cloning of nuclear proteins and nuclear
 RT targeting sequences on a functional basis."
 RL Anal. Biochem. 284:231-239(2000).

CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
 GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AJ388537; CAB52553.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPEROXDASE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KM Oxidoreductase; Peroxidase.
 FT NON_TER 98
 SQ SEQUENCE 98 AA; 10701 MW; 0BEFB0D612E9CF03 CRC64;

Query Match 4.8%; Score 9; DB 6; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFPCNOFG 90
 |||||||||
 DB 82 LAFPCNOFG 90

RESULT 10
 ID Q38703 PRELIMINARY; PRT; 116 AA.
 AC Q38703;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NONDOMANCY-ASSOCIATED CLONE AFN3 PUTATIVE ORF1 (FRAGMENT).
 OS Avena fatua.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Poace; Avena.
 OX NCBI_TaxID=4499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AN265; TISSUE=EMBRYO;
 RA Johnson R.R., Cranston H.J., Chaverra M.E., Dyer W.E.;
 RT "Characterization of cDNA clones for differentially expressed genes in
 RT embryos of dormant and nondormant Avena fatua caryopses."
 RL Plant Mol. Biol. 0:0-0(1995).
 DR EMBL: U20000; AAA6742.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPEROXDASE.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 116 AA; 13096 MW; 017AFD167116D975 CRC64;

Query Match 4.8%; Score 9; DB 10; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFPCNOFG 90
 |||||||||
 DB 15 LAFPCNOFG 23

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RESULT 11
O9SME4 PRELIMINARY: PRT: 165 AA.
ID O9SME4:
AC O9SME4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ALBOSTRIANS MUTANT LINE, AND CV. HAISA; TISSUE-LEAF;
RX MEDLINE=99439705; PubMed=10508912;
RA Chutin Y., Schilling S., Boerner T.;
RT "A gene family encoding glutathione peroxidase homologues in Hordeum
RT vulgare (Barley).";
RL FEBS Lett. 459:33-38(1999).
CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE + H(2)O(2) = OXIDIZED
CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
CC GLUTATHIONE + 2 H(2)O.
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
DR EMBL; AJ238745; CAB59895.1; -.
DR HSSP; P00435; 1GP1.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHpx; 1.
DR PRINTS; PR01011; GLUTPROXDASE.
DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
DR OXidoreductase; Peroxidase.
DR KW OXidoreductase; Peroxidase.
SQ SEQUENCE 165 AA; 18259 MW; 4EB0521711329F04 CRC64;

Query Match 4.8%; Score 9; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNOFG 90
DB 67 LAFCNOFG 75

RESULT 12
O48646 PRELIMINARY: PRT: 169 AA.
ID O48646:
AC O48646:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
GN TSC23.30 OR ATG411600.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98172218; PubMed=9511228;
RA Sugimoto M., Sakamoto W.;
RT "Putative phospholipid hydroperoxide glutathione peroxidase gene from
RT Arabidopsis thaliana induced by oxidative stress.";
RL Genes Genet. Syst. 72:311-316(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LANDSBERG ERECTA;

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RA Iers A., Burd S., Sonego L., Khalchitski A., Lomaniec E.;
RL Plant Physiol. 116:1193-1193(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-LANDSBERG ERECTA;
RA Bildeau P.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE + H(2)O(2) = OXIDIZED
CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
CC GLUTATHIONE + 2 H(2)O.
CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
DR EMBL; AB001568; BAA24226.1; -.
DR EMBL; AF030132; AAC09173.1; -.
DR EMBL; AL049500; CAB39331.1; -.
DR EMBL; AL041532; CAB78203.1; -.
DR HSSP; P00435; 1GP1.
DR ANU-2DPAGE; O48646; -.
DR InterPro: IPR000889; Glut_peroxidase.
DR Pfam; PF00255; GSHpx; 1.
DR PRINTS; PR01011; GLUTPROXDASE.
DR PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
DR PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
DR OXidoreductase; Peroxidase; Selenium; Selenocysteine.
DR FT BINDING 42 42
SQ SEQUENCE 169 AA; 18609 MW; E15F33A7FBB89DE4 CRC64;

Query Match 4.8%; Score 9; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNOFG 90
DB 67 LAFCNOFG 75

RESULT 13
O9FXS3 PRELIMINARY: PRT: 169 AA.
ID O9FXS3:
AC O9FXS3:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
GN NT-SUBC08.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]

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RP SEQUENCE FROM N.A.
 RA Takemoto D., Kawakita K.;
 RT "Molecular cloning of elicitor inducible genes of tobacco."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
 CC GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AB041518; BAB16430.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 KW Oxidoreductase; Peroxidase.
 SQ SEQUENCE 169 AA; 18785 MW; E01918069ED98A71 CRC64;

Query Match 4.8%; Score 9; DB 10; Length 169;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFPCNOFG 90
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 Db 68 LAFPCNOFG 76

RESULT 14
 024031 PRELIMINARY; PRT; 169 AA.
 AC 024031;
 DT 01-JAN-1998 (TREMUREL. 05, Created)
 DT 01-JAN-1998 (TREMUREL. 05, Last sequence update)
 DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
 GN GPXLF-1.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. VF88 MILL.;
 RX MEDLINE=98316667; PubMed=9654095;
 RA Depege N., Drevet J., Boyer N.;
 RT "Molecular cloning and characterization of tomato cDNAs encoding
 RT glutathione peroxidase-like proteins."
 RL Eur. J. Biochem. 253:445-451(1998).
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
 CC GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: Y14762; CAA75054.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 SQ SEQUENCE 169 AA; 18847 MW; 3686E83724467650 CRC64;

Query Match

4.8%; Score 9; DB 10; Length 169;

Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFPCNOFG 90
 |||||
 Db 68 LAFPCNOFG 76

RESULT 15
 049069 PRELIMINARY; PRT; 170 AA.
 ID 049069;
 AC 049069;
 DT 01-JUN-1998 (TREMUREL. 06, Created)
 DT 01-JUN-1998 (TREMUREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
 DE GLUTATHIONE PEROXIDASE (EC 1.11.1.9).
 OS Gossypium hirsutum (Upland cotton).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Malvales; Malvaceae; Gossypium.
 OX NCBI_TaxID=3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COCKER 312; TISSUE=IN VITRO COTTON OVULE CULTURE.
 RA Jaradat T.T., Allen R.;
 RT "Glutathione peroxidase from cotton, partial cDNA."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROTECTS CELLS AND ENZYMES FROM OXIDATIVE DAMAGE, BY
 CC CATALYSING THE REDUCTION OF HYDROGEN PEROXIDE, LIPID PEROXIDES AND
 CC ORGANIC HYDROPEROXIDE, BY GLUTATHIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 GLUTATHIONE + H(2)O(2) = OXIDIZED
 CC GLUTATHIONE + 2 H(2)O.
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
 CC ENCODED BY THE OPAL CODON, UGA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
 DR EMBL: AF037051; BAB94892.1; -.
 DR HSSP: P00435; IGPI.
 DR InterPro: IPR000889; Glut_peroxidase.
 DR Pfam: PF00255; GSHpx; 1.
 DR PRINTS: PR01011; GLUTPROXDAE.
 DR PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
 DR PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
 KW Oxidoreductase; Peroxidase.
 SQ SEQUENCE 170 AA; 18854 MW; 32FE5856B9B40F82 CRC64;

Query Match 4.8%; Score 9; DB 10; Length 170;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 LAFPCNOFG 90
 |||||
 Db 68 LAFPCNOFG 76

Search completed: August 23, 2002, 14:41:49
 Job time: 126 sec

